
* Note! Estimated insert size may differ from sequence length
 (see http://www.ncbi.nlm.nih.gov/pmc/books/PMC60/docs/Genbank_draft_data.html)

Note that this is a working draft; sequence it currently consists is a composite of the true order of the pieces as they were kept and their order in this sequence record as they vary. Gaps between the contents are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1338:	contig of 1338 bp in length
1339:	gap of unknown length
1439:	contig of 1080 bp in length
2619:	gap of unknown length
3438:	contig of 1220 bp in length
3938:	gap of unknown length
4952:	contig of 1314 bp in length
5352:	gap of unknown length
6817:	contig of 1465 bp in length
6818:	gap of unknown length
6918:	contig of 1551 bp in length
8469:	gap of unknown length
8569:	contig of 1249 bp in length
9819:	gap of unknown length
9919:	contig of 1407 bp in length
11354:	gap of unknown length
11424:	gap of unknown length
12930:	contig of 1406 bp in length
13030:	gap of unknown length
14031:	contig of 1018 bp in length
14034:	gap of unknown length
14049:	gap of unknown length
15102:	contig of 1154 bp in length
15149:	gap of unknown length
15402:	gap of unknown length
16871:	contig of 1469 bp in length
16971:	gap of unknown length
18532:	contig of 1541 bp in length
18632:	gap of unknown length
19679:	contig of 1367 bp in length
20079:	gap of unknown length
21993:	contig of 1914 bp in length
22093:	gap of unknown length
23145:	contig of 1367 bp in length
23545:	gap of unknown length
24821:	contig of 1276 bp in length
24921:	gap of unknown length
26547:	contig of 1626 bp in length
26647:	gap of unknown length
28123:	contig of 1476 bp in length
28223:	gap of unknown length
29473:	contig of 1210 bp in length
29573:	gap of unknown length
30773:	contig of 1138 bp in length
32694:	contig of 1927 bp in length
32798:	gap of unknown length
34374:	contig of 1576 bp in length
34474:	gap of unknown length
34574:	contig of 2162 bp in length
36736:	gap of unknown length
38237:	contig of 2101 bp in length
39937:	gap of unknown length
40214:	contig of 1277 bp in length
40314:	gap of unknown length
41236:	contig of 1447 bp in length
41906:	gap of unknown length
43552:	contig of 1646 bp in length
43652:	gap of unknown length
45266:	contig of 1614 bp in length
45366:	gap of unknown length
47335:	contig of 1967 bp in length
47433:	gap of unknown length
49508:	contig of 2075 bp in length
49608:	gap of unknown length
53427:	contig of 2719 bp in length

52328	52427:	gap	of unknown length
52428	52428:	cont ig	of 1397 bp in length
53623	53623:	gap	of unknown length
53925	53925:	cont ig	of 1454 bp in length
55279	55279:	gap	of unknown length
55379	55379:	cont ig	of 2446 bp in length
57725	57724:	gap	of unknown length
57825	59561:	cont ig	of 1737 bp in length
59562	59561:	gap	of unknown length
61510	61510:	cont ig	of 1547 bp in length
61610	61610:	gap	of unknown length
63952	63952:	cont ig	of 2442 bp in length
63953	64052:	gap	of unknown length
64053	67489:	cont ig	of 3437 bp in length
67490	67583:	gap	of unknown length
67590	71050:	cont ig	of 3461 bp in length
71051	71150:	gap	of unknown length
74151	74048:	cont ig	of 2898 bp in length
74049	74148:	gap	of unknown length
74149	77038:	cont ig	of 2890 bp in length
77039	77138:	gap	of unknown length
77139	79459:	cont ig	of 2421 bp in length
79460	80559:	gap	of unknown length
79560	82698:	cont ig	of 3139 bp in length
82699	82758:	gap	of unknown length
82759	85025:	cont ig	of 2237 bp in length
85026	85125:	gap	of unknown length
85126	88657:	cont ig	of 3532 bp in length
88658	88757:	gap	of unknown length
88758	94354:	cont ig	of 4407 bp in length
94355	93264:	gap	of unknown length
93265	93865:	cont ig	of 2506 bp in length
93866	95960:	gap	of unknown length
95961	98791:	cont ig	of 2831 bp in length
98792	98891:	gap	of unknown length
98892	103892:	cont ig	of 5001 bp in length
103893	103992:	gap	of unknown length
103993	107044:	cont ig	of 3052 bp in length
107045	107344:	gap	of unknown length
107346	111412:	cont ig	of 4208 bp in length
111413	111512:	gap	of unknown length
111513	115079:	cont ig	of 5563 bp in length
115079	115175:	gap	of unknown length
115176	118661:	cont ig	of 5486 bp in length

Query Match	11.6%	Score 157.2;	DB 2;	Length 1619257
Best Local Similarity	79.5%	Pred. No. 9.8e+26;		
Matches	486	Conservative	0	Mismatches 48
				Indels 0

[illegible]

Search completed: January 12, 2003, 01:11:45
Job time : 2906.18 secs

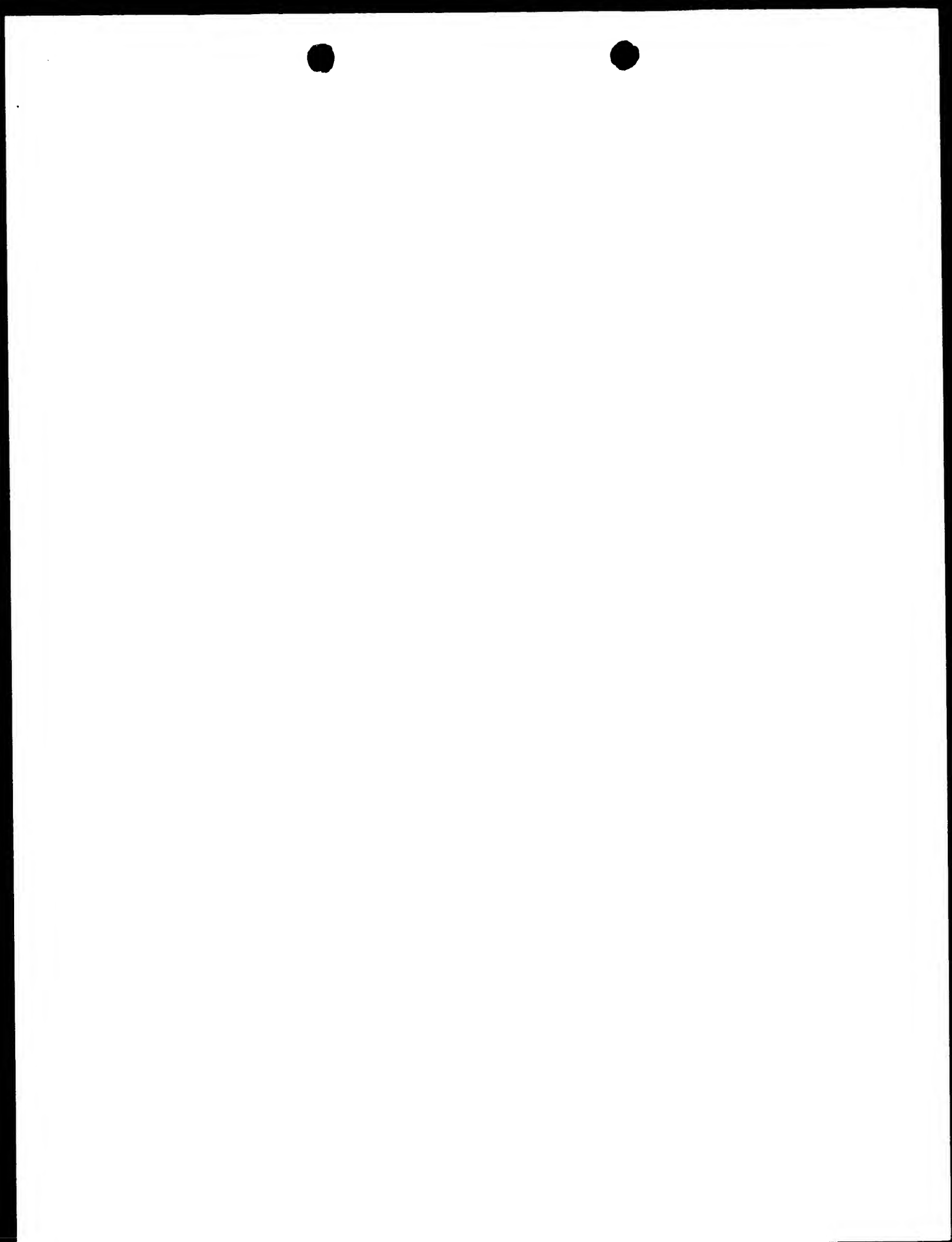
[illegible][illegible]

Mon Jan 13 09:24:13 2003

us-09-864-711-8.rng

Page 13

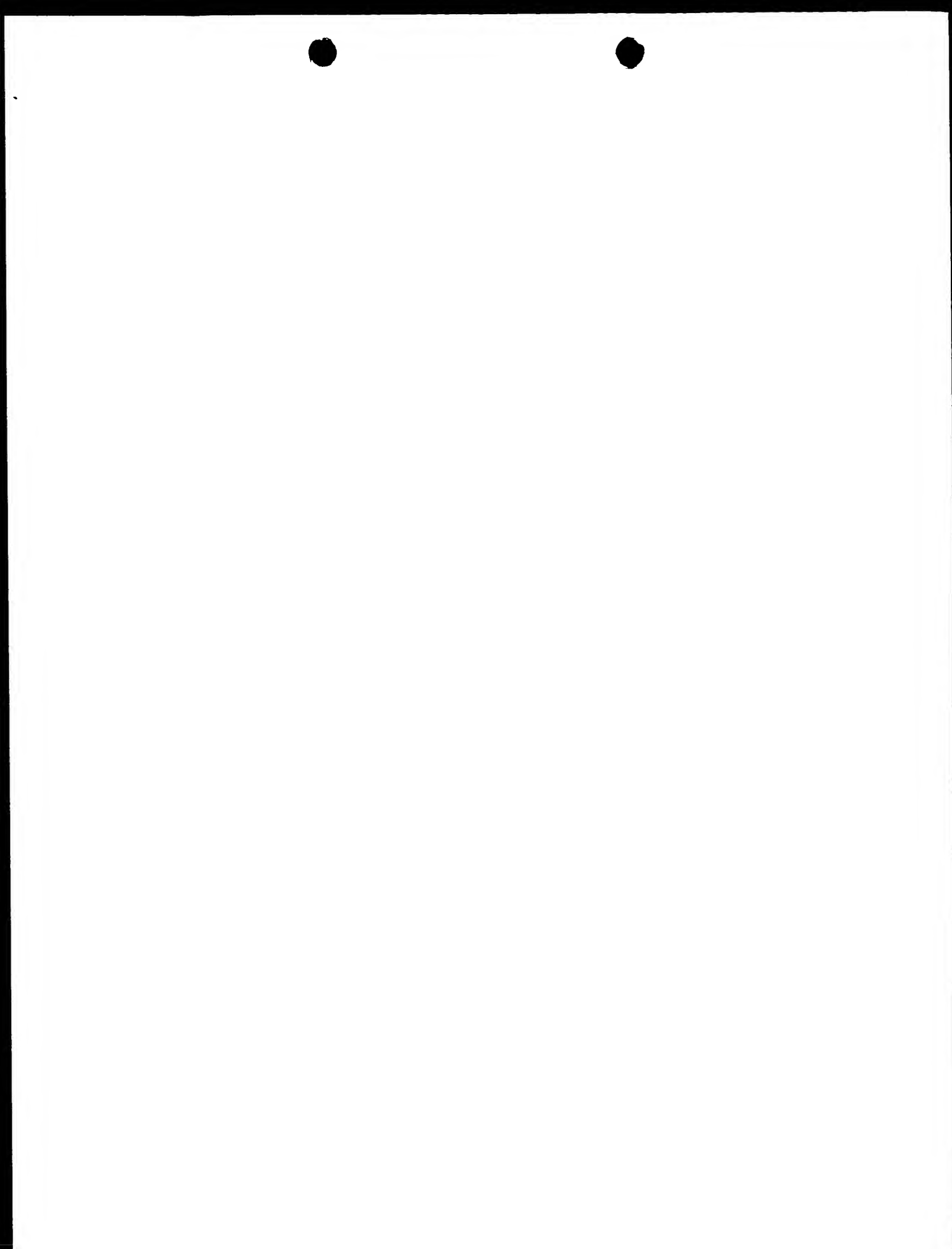
Job time : 206.731 secs



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1



[illegible][illegible]


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Query Matched: 5 7 % Score 99.41 DB 101 Length 10271
Best local similarity: 51.7% Best No. 6,48,189
Matches 241: conservative 0: Mismatch 10: Gaps

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Query: March 10, 2017 Score: 95.4; DB: 10; Length: 753;
Best Local Similarity: 50.2%; Pred. No.: 5,6e-17;
Marches: 106; Conservative: 1; Mismatches: 27; Indels: 15; Gaps: 2;

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Original clone citation: National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
This read has been verified (found to hit its original self in the cancer orientation)

Insert Length: 1464 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 460.

COMMENT

Source: 3201 Carnegie Ave., Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scanlab@therys.com

FEATURES

Source

High quality sequence stop: 488.
Location/Qualifiers
1..641
/organism="Homo sapiens"
/db="GenBank" accession="AF060606"
/clone_lib="Atherys RAGE Library"
/cell_line="H1080"
/note="Spec. Creation of Genom-wide Protein Expression Libraries using Random Activation of Gene Expression. Nature Biotechnology, in press. Note that even though the cell type indicated is H1080, since a random activation method was used, these sequences may not necessarily be expressed in H1080 under normal circumstances."
1..641
1..641
1..641

Query Match

Best local similarity: 43.6%; Score: 594.6; DB: 10; Length: 641
Matches: 611; Conservative: 0; Mismatches: 10; Indels: 1; Gaps: 1

FEATURES

Source

High quality sequence stop: 535.
Location/Qualifiers
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/organism="Homo sapiens"
/db="GenBank" accession="AF060606"
/clone_lib="Atherys RAGE Library"
/cell_line="H1080"
/note="Spec. Creation of Genom-wide Protein Expression Libraries using Random Activation of Gene Expression. Nature Biotechnology, in press. Note that even though the cell type indicated is H1080, since a random activation method was used, these sequences may not necessarily be expressed in H1080 under normal circumstances."
1..641
1..641
1..641

Query Match

Best local similarity: 43.6%; Score: 591; DB: 10; Length: 641
Matches: 611; Conservative: 0; Mismatches: 15; Indels: 1; Gaps: 1

FEATURES

Source

High quality sequence stop: 535.
Location/Qualifiers
1..641
/organism="Homo sapiens"
/db="GenBank" accession="AF060606"
/clone_lib="Atherys RAGE Library"
/cell_line="H1080"
/note="Spec. Creation of Genom-wide Protein Expression Libraries using Random Activation of Gene Expression. Nature Biotechnology, in press. Note that even though the cell type indicated is H1080, since a random activation method was used, these sequences may not necessarily be expressed in H1080 under normal circumstances."
1..641
1..641
1..641

Query Match

Best local similarity: 43.6%; Score: 591; DB: 10; Length: 641
Matches: 611; Conservative: 0; Mismatches: 15; Indels: 1; Gaps: 1

FEATURES

Source

High quality sequence stop: 535.
Location/Qualifiers
1..641
/organism="Homo sapiens"
/db="GenBank" accession="AF060606"
/clone_lib="Atherys RAGE Library"
/cell_line="H1080"
/note="Spec. Creation of Genom-wide Protein Expression Libraries using Random Activation of Gene Expression. Nature Biotechnology, in press. Note that even though the cell type indicated is H1080, since a random activation method was used, these sequences may not necessarily be expressed in H1080 under normal circumstances."
1..641
1..641
1..641

